Toll-like receptor evolution in birds: gene duplication, pseudogenisation and diversifying selection

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Toll-like receptor evolution in birds: gene duplication, pseudogenisation and diversifying selection.

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Abstract

Toll-like receptors (TLRs) are key sensor molecules in vertebrates triggering initial phases of immune responses to pathogens. The avian TLR family typically consists of ten receptors, each adapted to distinct ligands. To understand the complex evolutionary history of each avian TLR, we analysed all members of the TLR family in the whole genome assemblies and target sequence data of 63 bird species covering all major avian clades. Our results indicate that gene duplication events most probably occurred in TLR1 before synapsids diversified from sauropsids. Unlike mammals, ssRNA-recognising TLR7 has duplicated independently in several avian taxa, while flagellin-sensing TLR5 has pseudogenised multiple times in bird phylogeny. Our analysis revealed stronger positive, diversifying selection acting in TLR5 and the three-domain TLRs (TLR10 [TLR1A], TLR1 [TLR1B], TLR2A, TLR2B, TLR4) that face the extracellular space and bind complex ligands than in single-domain TLR15 and endosomal TLRs (TLR3, TLR7, TLR21). In total, 84 out of 306 positively selected sites were predicted to harbour substitutions dramatically changing the amino acid physicochemical properties. Furthermore, 105 positively selected sites were located in the known functionally-relevant TLR regions. We found evidence for convergent evolution acting between birds and mammals at 54 of these sites. Our comparative study provides a comprehensive insight into the evolution of avian TLR genetic variability. Besides describing the history of avian TLR gene gain and gene loss, we also

identified candidate positions in the receptors that have been likely shaped by direct molecular host-pathogen co-evolutionary interactions and most probably play key functional roles in birds.

Introduction

The species richness and wide range of ecological adaptations are remarkable in birds (Jetz et al. 2012). Despite being similar to mammals in many aspects of their biology, birds evolved many similar traits (including homoiothermy and parental care) convergently through their analogous ecological life strategies (Farmer 2000; Emery and Clayton 2004; Olkowicz et al. 2016; Lovegrove 2017). Recent advance in avian genomic research, which started with the Avian Phylogenomics Project (http://avian.genomics.cn/en/; Zhang et al. 2014a) and continues with the Bird 10,000 Genomes Project (https://b10k.genomics.cn/) has created new possibilities to use publicly available whole genome sequencing data to resolve many questions regarding avian biology, evolution and adaptations (Zhang et al. 2014b). Among these, the evolution of avian immune function is of particular interest. Being challenged by similar classes of pathogens as found in mammals, highly diversified immune genes in birds are rich in mixed signatures of symplesiomorphy, convergence and apomorphic adaptations to novel functions (Burri et al. 2010; Cheng et al. 2015).

The co-evolution between host and pathogen likely involves mainly molecules that form direct interface between the host and the pathogen structures e.g. the pattern recognition receptors (PRRs) and their ligands, the pathogen-associated molecular patterns (PAMPs; Janeway and Medzhitov 2002). Forming the first line of the host immune defence, PRRs appear to constantly evolve towards specific and appropriate recognition of certain PAMPs (Wang et al. 2016b). The Toll-like receptor (TLR) protein family belongs to one of the most essential and functionally most characterised PRRs (Palm and Medzhitov 2009; Coscia et al. 2011). After specific PAMP binding, TLRs trigger signalling pathways activating transcription factors, such as NF-κB to induce expression of target genes that are key to triggering an inflammatory immune response and subsequent activation of acquired immunity (Iwasaki and Medzhitov 2015).

TLRs are transmembrane proteins each with the characteristic horse-shoe-shaped ectodomain (ECD), where the direct contact between the receptor surface and specific microbe molecules occurs, the transmembrane domain and an intracellular Toll–interleukin 1 receptor (TIR) domain that enables the downstream signal transmission (Kawai and Akira 2010). The capacity to bind a particular type of ligand in TLRs is dependent on the structure of the ECD. This has been used to divide the vertebrate TLRs into three different groups based on the pattern of hydrogen-bonds formed among the asparagine residues in the neighbouring leucine-rich repeats, which stabilise the shape of the ECD

(Wang et al. 2016b). The ten avian TLR family members belong either to the single-domain TLRs possessing a complete asparagine ladder (TLR3, TLR5, TLR7, TLR15 and TLR21) or to the three-domain TLRs with the ladder interrupted in the central part of the ECD (TLR1A, TLR1B, TLR2A, TLR2B and TLR4; Wang et al. 2016b). While some avian TLRs conservatively recognise the same ligands as mammalian TLRs (such as TLR4 detecting bacterial lipopolysaccharides, LPS; TLR5 flagellin; TLR3 dsRNA or TLR7 ssRNA; reviewed by Keestra et al. 2013), others were reported to form distinct paralogues with related ligand specificity (e.g. heterodimer-forming TLR1A/TLR1B together with TLR2A/TLR2B, which recognise di/triacylated lipopeptides; Keestra et al. 2007; Higuchi et al. 2008) or achieve recognition of similar ligands as their mammalian analogues through convergence (e.g. avian TLR21 that recognises CpG DNA similarly as mammalian TLR9; Brownlie et al. 2009; Keestra et al. 2010). Finally, TLR15 that is unique to birds evolved to gain a novel function in recognition of extracellular proteases (de Zoete et al. 2011).

Gene duplication is an important mechanism allowing genes to evolve novel functions (Zhang 2003; Ellegren 2008). Gene duplications are common in TLRs, as with other immune genes. Duplicated TLR1 family members are known in mammals (TLR1, TLR6, TLR10 and TLR2) as well as in birds (TLR1A, TLR1B, TLR2A and TLR2B; Coscia et al. 2011; Huang et al. 2011; Wang et al. 2016b). Recently, duplication of *TLR7* has been described in several avian taxa (Cormican et al. 2009; Grueber et al. 2012; Raven et al. 2017), while other birds possibly lack the duplicated *TLR7*. This intriguing finding contrasts with that found in mammals, which contain two other TLR7-like family members, *TLR8* and *TLR9*, both missing in birds (Philbin et al. 2005; Temperley et al. 2008), suggesting that gene loss may also play a significant role in avian TLR evolution. *TLR5* pseudogenisation occurred independently several times within the passerines (Bainova et al. 2014) and possibly in parrots (Alcaide and Edwards 2011). The general pattern of *TLR* pseudogenisation and gene duplication is largely unknown and may be far more common across various *TLR* genes and avian taxa.

Although generally conserved in their structure, TLRs were reported to exhibit very high levels of inter- and intra-specific genetic variation in birds (Alcaide and Edwards 2011; Huang et al. 2011; Grueber et al. 2014). Several authors have documented the functional significance of TLR genetic variation (Leveque et al. 2003; Walsh et al. 2008), characterised associations between TLR variation and disease susceptibility (Netea et al. 2012; Medvedev 2013) and suggested the maintenance of intraspecific polymorphism through balancing selection mediated by pathogens (Ferrer-Admetlla et al. 2008). Despite several attempts to understand the evolutionary significance of TLR genetic variation in birds (Alcaide and Edwards 2011; Grueber et al. 2014; Vinkler et al. 2014), the question of its adaptive value for avian specific PAMP recognition remains unresolved. Here we use various

approaches to analyse natural selection in the most comprehensive attempt to investigate adaptive pathogen-driven evolution in avian TLRs.

Facilitated by the conservative structures of TLR molecules, they present a suitable model for studying pathogen-driven micro-evolutionary processes at the DNA level. The direct contact between TLRs and PAMPs is restricted to certain amino acid sites (Gay and Gangloff 2007) where even single amino acid substitutions may have profound effects on receptor binding properties (e.g. Keestra et al. 2008; Walsh et al. 2008; Resman et al. 2009; Meng et al. 2010). Thus, positively selected sites can be predicted to emerge from the generally negatively selected background and can be used for prediction of functionally relevant positions in non-model animals lacking precise protein crystallographic data. Several studies have investigated the nature of positively selected sites (PSS) at the interspecific level in various TLRs in selected bird taxa (Alcaide and Edwards 2011; Huang et al. 2011; Grueber et al. 2014; Vinkler et al. 2014; Wang et al. 2016b). Yet, co-location study of PSS on the receptor surface with the predicted functional residues already known in the model species (human and mouse), has never been done across the avian phylogeny (but see Vinkler et al. 2014, for a similar approach in Galloanserae birds).

Given the current lack of comprehensive evidence on TLR family molecular evolution across the avian phylogeny, our comparative study reported here performed evolutionary analysis on whole-genome sequences for 48 species representing 34 avian orders (Supplementary Material 2: Table S23) mainly gained through the Avian Phylogenomics Project (Zhang et al. 2014a). The TLR sequences extracted from these genomes together with those added from other public resources (in total 63 species) allowed us to infer the history of avian *TLR* gene gain and gene loss in the context of TLR evolution in other vertebrates. By critical assessment of positive selection acting on all members of the TLR family in birds we describe the adaptive micro-evolutionary changes in these immune receptors in their molecular context. Thus, this study is the first to comprehensively predict functionally relevant genetic variation in avian TLRs providing insights into the co-adaptation between host and pathogen through evolution of ligand recognition.

Results and Discussion

Evolution of *TLR1* family gene duplications

The *TLR1* gene family is widely duplicated in vertebrates including birds (*TLR1A*, *TLR1B*, *TLR2A* and *TLR2B*; Temperley et al. 2008; Cormican et al. 2009; Huang et al. 2011; Wang et al. 2016b). Presently, however, the timing of these gene duplication events is unclear: the paralogues within the *TLR1* and *TLR2* subfamily were suggested to have duplicated before the mammalian divergence from

sauropsids (Huang et al. 2011) or after this divergence, independently in birds and mammals (Temperley et al. 2008; Cormican et al. 2009; Mikami et al. 2012; Wang et al. 2016b). This disagreement results from the lack of accounting for gene conversion as a mechanism of paralogue sequence homogenisation in some studies (Temperley et al. 2008; Cormican et al. 2009; Wang et al. 2016b). We found significant support for gene conversion between the two paralogues both in the *TLR1* subfamily (*TLR1A* and *TLR1B*) and *TLR2* subfamily (*TLR2A* and *TLR2B*; Supplementary Material 1: Table S1; for detailed info see Supplementary Material 3) in birds. Therefore, we constructed both *TLR1* and *TLR2* phylogenetic trees based on the protein sequences of the non-converted regions only (Fig. 1; Supplementary Material 1: Fig. S1 and Fig. S2).

Our results based on the analysis of 179 sequences of 83 vertebrate species (for the list see Supplementary Material 2: Table S24) show that in the *TLR1* family the sequences of avian species cluster together based on paralogue identity (Supplementary Material 1: Fig. S1). Avian *TLR1A* and reptilian *TLR10* cluster together with mammalian *TLR10*, while avian *TLR1B* and reptilian *TLR1*/*TLR6* (inconsistent nomenclature in reptilian *TLR1*) cluster together with mammalian *TLR1* and *TLR6* paralogues (shown in Fig. 1; detailed in Supplementary Material 1: Fig. S1). This is consistent with the results previously published by Huang et al. (2011) confirming that the first duplication event within the *TLR1* subfamily occurred before mammal-reptile divergence. On the basis of these findings we suggest renaming avian *TLR1A* to *TLR10* (from now on marked as *TLR10* [*TLR1A*] in the text), while modifying the name of the avian *TLR1B* gene to *TLR1* (marked as *TLR1* [*TLR1B*]). Our analysis also indicates that the duplication of *TLR1* in amphibians (namely in *Xenopus*) apparently arose independently of the *TLR1* duplication in amniotes (Supplementary Material 1: Fig. S1).

Also, in the *TLR2* subfamily there are two copies present in birds (*TLR2A* and *TLR2B*). In mammalian genomes, on the other hand, only one functional *TLR2* is maintained and for some species *TLR2-like* pseudogenes (a second copy) were described (Roach et al. 2005). The duplication of *TLR2* in sauropsids could have arisen independently of mammals, or alternatively, a duplication event pre-dating divergence between birds and mammals could have occurred (similar to the *TLR1* subfamily), followed with pseudogenisation leaving only a single *TLR2* copy in mammals (Huang et al. 2011). Our analysis of 137 homologous sequences in 78 vertebrate species (for the list see Supplementary Material 2: Table S24) contradicts the second scenario (Supplementary Material 1: Fig. S2) and supports the independent duplication of *TLR2* in sauropsids. This is also supported by the phylogenetic analysis of a ca. 80 amino-acid-long alignment of the conserved sequence in human *TLR2*/*TLR2-like* pseudogene and chicken TLR2A/TLR2B (Supplementary Material 1: Fig. S3); the resulting phylogenetic tree suggests that *TLR2* duplication in birds was independent of a parallel

mammalian *TLR2* duplication that was followed by a pseudogenisation of the second *TLR2* copy (Supplementary Material 1: Fig. S4). However, it is difficult to draw any final conclusions on the validity of the two scenarios proposed for *TLR2* evolution in amniotes since the support for the branching of the avian *TLR2* paralogues is limited (bootstrap support for the mammal-sauropsid split = 47, Supplementary Material 1: Fig. S2).

Avian *TLR7* gene duplications

Birds lack two of the three vertebrate *TLR7* family members (i.e. *TLR8* and *TLR9*; Philbin et al. 2005; Temperley et al. 2008). Instead, the avian *TLR7* locus appears to have recently duplicated in some passerines (Cormican et al. 2009; Grueber et al. 2012) and waders (Raven et al. 2017). Within the genome sequences investigated in this study we also found two *TLR7* copies in other avian taxa: Cuculiformes and Mesiornithiformes (Fig. 2). The number of amino acid substitutions distinguishing the two *TLR7* loci ranges between species from 21 in zebra finch (*Taeniopygia guttata*) to only 3 in rifleman (*Acanthisitta chloris*; see Fig. 2; Supplementary Material 1: Table S2 and Supplementary Material 4). Furthermore, the two *TLR7* copies likely differ slightly in their functions, because 11 of the sites identified as distinct between the two copies in any avian species match the known ligand-binding positions (Wei et al. 2009; Gupta et al. 2016; Zhang et al. 2016), five are situated in the Z-loop region responsible for ligand binding and dimerization and the other 10 variable sites are identical with PSS detected in birds (Supplementary Material 1: Table S3). To bring independent support to the evidence of *TLR7* gene duplication we performed a PCR-based quantitative copy number variation (CNV) analysis comparing *TLR7* with two single-copy *TLRs* (*TLR3* and *TLR4*) in selected species (collared flycatcher, *Ficedula albicollis*; ground tit, *Pseudopodoces humilis*; white-throated sparrow, *Zonotrichia albicollis* and zebra finch). Our results confirm that the zebra finch (a species with two *TLR7* loci based on the genome sequence analysis) possesses two *TLR7* copies (Supplementary Material 1: Table S4, Table S5, Table S6 and Fig. S5), while the other investigated species (with a predicted single *TLR7* locus) possess only one *TLR7* gene copy. In contrast to the *TLR1* family, we did not detect any gene conversion between the two copies of the duplicated *TLR7* genes (see Supplementary Material 3). Despite this, the constructed tree of avian TLR7 does not show any evidence of two separate TLR7 phylogenetic clusters, but surprisingly both copies of *TLR7* always clustered separately for each species (Supplementary Material 1: Fig. S6 and Table S7). Therefore, we infer that the duplication in *TLR7* occurred several times independently in recent avian history and possibly even multiple times in some cases (as e.g. in ruddy turnstone, *Arenaria interpres,* where *TLR7* was reported to be triplicated; Raven et al. 2017).

TLR5 pseudogenisation in birds

Recently, it has been shown that there is no functional gene for TLR5 in some passerine species (Bainova et al. 2014). In this study we have also found several avian taxa possessing only non-functional *TLR5* pseudogenes with stop-codons in their sequences. Apart from passerines we revealed *TLR5* pseudogenes in other clades: i.e. Psittaciformes, Cariamiformes, Trogoniformes, Phaethontiformes, Eurypygiformes and Apodiformes (Fig. 3). The sequence data show that the stop-codon positions differ among the investigated species with differences also in the pseudogenisation mechanism (single nucleotide substitution or frame-shifting indels, see Supplementary Material 1: Table S8). The stop-codons in *TLR5*, thus, arose independently in the evolutionary history of the different avian taxa. This, however, does not appear to be the result of relaxed selection acting in *TLR5*. Firstly, the number of single nucleotide variants (SNVs) in the alignment of the *TLR5* functional sequences is comparable to other *TLRs* (indicating comparable mutation rate; Supplementary Material 1: Table S9). Secondly, the total number of PSS is higher than in other TLRs and ω (dN/dS ratio) is again similar to other TLRs (see below and Supplementary Material 1: Table S10) and higher than the genome average (Zhang et al. 2014b). However, since most of the PSS contain only conservative substitutions without dramatic effects on the amino acid site physicochemical properties, it appears that negative selection may prevent the loss of function in those species where the *TLR5* functional gene is maintained. Altogether this suggests that there may be a selection for TLR5 loss of function in certain avian evolutionary lineages. The loss of a *TLR5* functional gene is not limited only to birds. The *TLR5* pseudogene has also been described in one human allele, where its presence is associated with an increased risk of pneumonia infection caused by flagellated bacteria *Legionella pneumophila* (Hawn et al. 2003; Zhang et al. 2013), while at the same time possessing a *TLR5* non-functional allele might be advantageous for decreasing the probability of autoimmune disease development (Hawn et al. 2005). *TLR5* pseudogenisation may be allowed by the high redundancy of pathogen detection, where apart from TLR5, flagellin is also recognised by other PRRs e.g. NLRC4 inflammasome (Zhao et al. 2011; Yang et al. 2014). In birds other flagellin-recognising PRRs have not yet sufficiently been studied to support this hypothesis.

Diversifying selection in avian TLRs

We tested pervasive, positive and diversifying selection acting in all avian TLRs. Numbers of PSS differ between *TLRs* (from 0.3% to 5.8% PSS per TLR; Table 1; Supplementary Material 1: Fig. S7 and Supplementary Material 5: Table S26). The results suggest that positive selection is acting more on TLRs exposed towards the cell surface (mainly TLR1 [TLR1B], TLR2A, TLR5, TLR4 and TLR2B), than in the TLRs situated in endosomes (TLR21, TLR3 and TLR7). This may be because the endosomal TLRs

are specialised for detection of less complex ligands, which show low structural variation (such as ssRNA in TLR7, dsRNA in TLR3 or CpG DNA regions in TLR21; Brownlie and Allan 2011) interacting with the genetic variability in TLRs. This supports the previous findings by Mikami et al. (2012) in vertebrates. The only exception is TLR15, which is unique to birds and reptiles (Boyd et al. 2012). Although situated on the cell surface, TLR15 is activated (unlike other TLRs) by the ECD proteolytic cleavage with pathogen-derived proteases (de Zoete et al. 2011). Since *TLR15* harbours only low numbers of PSS (Table 1), we hypothesise that this pathogen-recognition mechanism may be linked to reduced positive selection acting on the ECD. Nonetheless, the cleavage site is variable across bird taxa and contains two PSS (Supplementary Material 1: Table S11; see also Supplementary Material 1: Text S1 and Fig. S8).

Our results are also mostly consistent with the findings of Wang et al. (2016b), who suggested grouping of TLRs based on their ECD architecture and showed that in mammals the single-domain TLRs (TLR3, TLR5, TLR7, TLR15 and TLR21) are under stronger purifying selection than the three-domain TLRs (TLR10 [TLR1A], TLR1 [TLR1B], TLR2A, TLR2B and TLR4). Here we found that also in birds the positive selection is acting more on the three-domain TLRs, with the exception of TLR5, which is under strong positive selection in birds (Table 1 and Supplementary Material 1: Fig. S7). Since some avian species have lost a functional TLR5 through pseudogenisation (Bainova et al. 2014; and this study, Fig. 3), we hypothesise that TLR5 has a specific role in avian immunity when compared, for example, to mammals. The variation in selection acting at TLR5 in different taxa might, for example, reflect the differences in selection against overactivation of gut immunity with flagellated symbiotic microbiota (Iqbal et al. 2005).

Being responsible for direct and specific recognition of structurally heterogeneous PAMPs (Reddick and Alto 2014), the pathogen-mediated selective pressures are particularly diversified in the TLR ECDs. As previously shown in general for vertebrates (Mikami et al. 2012), we also find the majority of TLR PSS in birds to be situated in ligand-binding ECDs (Supplementary Material 1: Fig. S7; the exact positions of PSS are visualised in Supplementary Material 1: Fig. S9 and listed in Supplementary Material 6: Table S27). We may predict stronger functional effects of PSS with non-conservative amino acid substitutions that change the physicochemical properties of the particular residues. The highest numbers of these non-conservative PSS are in TLR4 and TLR2A (Fig. 4; see also Supplementary Material 1: Table S12; Supplementary Material 7 and Supplementary Material 8). Especially in TLR4, most PSS with dramatic changes in charge and hydrophobicity fall into the known functionally important sites of the receptor, with high probability of changing the TLR4 ligand-binding properties. On the other hand, most substitutions in PSS in TLR15, TLR3, and TLR10 [TLR1A] do not

significantly change the amino acid physicochemical properties. Despite avian TLR1 [TLR1B] being significantly shorter than TLR10 [TLR1A], we found more PSS in TLR1 [TLR1B] and these were less conservative in their charge than in TLR10 [TLR1A], especially in the predicted ligand-binding region that is spanning the region avoiding gene conversion (Supplementary Material 1: Text S2; Supplementary Material 7). This, together with high TLR2A PSS variation, can be possibly explained by distinct binding capacities of the heterodimers formed by the duplicated TLR1/TLR2 subfamily members, where the combination TLR1 [TLR1B]/TLR2A (unlike any other combination) is able to recognise peptidoglycans and efficiently recognises diacylated bacterial lipoproteins (BLP; Higuchi et al. 2008). Surprisingly, despite its high number of PSS, TLR5 is the most PSS-conservative TLR across all avian taxa (Supplementary Material 1: Table S12). Given that flagellin is the only known TLR5 ligand (Hayashi et al. 2001), this may indicate functional constraints in those species with preserved functional TLR5, limiting any adaptations to larger numbers of relatively minor changes. The PSS identified in this study are consistent with PSS identified by other studies and other taxa especially in TLR15, TLR4 and TLR5 (PSS listed in Supplementary Material 6: Table S27 and those located in ECD visualised in Fig. 5; visualisation of ECDs along with intracellular domains, ICDs, and transmembrane, TM, regions is given in Supplementary Material 9). Interestingly, from the five amino acid substitutions related to *Salmonella enterica* resistance variation in chickens (Leveque et al. 2003) only position E301 is also positively selected within birds in general, where negatively charged E/D are substituted with positively charged K/R (Fig. 4). The relevance of this position was also supported in other studies of birds (Grueber et al. 2014) and mammals (Vinkler et al. 2009; Wlasiuk and Nachman 2010) and partially with the results of numerous human studies (Arbour et al. 2000; Zareparsi et al. 2005; Shen et al. 2010; Cario 2013; Rupasree et al. 2015; but see also Ohto et al. 2012b) showing potential importance of variation at a neighbouring position D299G (D303 in chicken sequence).

We found the highest agreement between the PSS and known functional site distribution in TLR5, TLR4, TLR2A and TLR1 [TLR1B] (23, 18, 18 and 16 positions, respectively; for details see Supplementary Material 1: Table S13 and Fig. S10). We show that the PSS frequently evolve towards an amino acid of similar physicochemical properties being gained in distantly related avian taxa, while distinct properties can be found in closely related taxa (Supplementary Material 1: Text S2; Supplementary Material 8). This convergent evolution may result from analogous selective pressures induced by partially similar microbial communities in different avian taxa (Waite and Taylor 2014). For example, there are several PSS in avian TLR4 (D345, E375 and G379) that are good candidates for functionally important sites evolving under convergence either towards negative or towards positive

charge (Supplementary Material 8). Being either lipid IVa-binding sites (Meng et al. 2010; Ohto et al. 2012a; Scior et al. 2013) or LPS-binding sites (Park et al. 2009; Garate and Oostenbrink 2013; Paramo et al. 2013; Scior et al. 2013), these positions have been identified as positively selected also in several other studies in birds (Grueber et al. 2014) and mammals (Nakajima et al. 2008; Vinkler et al. 2009; Wlasiuk and Nachman 2010; Areal et al. 2011; Shen et al. 2012; Fornuskova et al. 2013).

The lack of agreement between the identified PSS and previously described TLR functional sites in other TLRs may be caused either by the lack of functional studies in some TLRs (e.g. TLR15 and TLR21) or by interspecific variation in TLR-ligand binding (e.g. TLR1, TLR3 and TLR7, where the structural and experimental studies were performed in mammals and not in birds; see Supplementary Material 1: Text S2). In both cases the analysis of PSS may indicate the target sites that are candidates for a functional role and may be the focus for further research. Despite the low number of PSS among the previously reported functional sites of TLR7, which may result from the constraints of conservative ligand binding, two non-conservative PSS located on the TLR7 Z-loop at the proximity of the TLR7 cleavage site (Supplementary Material 1: Text S2; Ewald et al. 2008; Kanno et al. 2013) might affect formation of secondary ligand-binding sites (Zhang et al. 2016).

Although most of the PSS functional sites are located in the ECD and involved in direct ligand binding, in TLR3 we found two PSS that are lying in the transmembrane region and are located in close proximity to the known receptor dimerization residues (Fig. 4). Since TLR3 dimerization depends on the dsRNA length (Pirher et al. 2008) and the number of TLR3 molecules involved in the interaction (TLR3 dimer or trimer; Mineev et al. 2014), selection on these residues may play a crucial role in ligand recognition in TLR3. In general, however, most PSS in avian TLR3 are very conservative (Fig. 4; for details see also Supplementary Material 1: Table S12 and Supplementary Material 7), which is consistent with the results reported by Wang and colleagues (Wang et al. 2016b) who identified the TLR3 family as the most conservative TLR family within vertebrates. The avian PSS which can be suggested as candidates for relevant functional effect based on the non-conservativeness of the changes in their physicochemical properties are described in Supplementary Material 1: Text S2.

Conclusions

To our knowledge, this is the first study investigating adaptive evolution in all members of the avian TLR protein family in high number of species and most avian orders. Although we were unable to extract data to all TLR genes from all avian whole-genome assemblies investigated, our study covers 87% of the genes in these species, providing the most comprehensive analysis published so far. Our results provide important novel insights into the history of TLR family evolution including the processes of diversifying selection, pseudogenisation and gene duplication. Most importantly, we

show that the main duplication event for *TLR1* arose before avian and mammalian lineages split into separate clades (giving rise to *TLR1* [avian *TLR1B*] and *TLR10* [avian *TLR1A*]), while avian gene duplication of *TLR2* to *TLR2A* and *TLR2B* may have occurred in parallel to *TLR2* duplication in some mammals that resulted in pseudogenisation of the second copy of *TLR2*. The latter conclusion however remains uncertain due to the power limitation imposed by the short sequences (not affected by gene conversion) aligned in our analysis. Furthermore, we confirmed the unique avian gene duplication in *TLR7* based on qPCR copy-number variation analysis. Surprisingly, this recent *TLR7* gene duplication in birds emerged independently in many species and representing several clades (Passeriformes, Charadriiformes, Cuculiformes and Mesiornithiformes). Similarly, the *TLR5* pseudogenisation, previously reported in several passerines and parrots, is seemingly more widespread in birds. Independent loss of functional TLR5 occurred also in seriemas (Cariamiformes), trogons (Trogoniformes), tropicbirds (Phaethontiformes), sunbitterns (Eurypygiformes) and swifts (Apodiformes).

The results of our analysis of positive selection in avian TLRs allowed us to predict functionally important, interspecifically variable positions. Consistent with some previous findings, these sites were located mainly at the ligand binding extracellular domain, mostly in TLRs where the extracellular domain is exposed to the cell surface and binds structurally diverse ligands (mainly in TLR1 [TLR1B], TLR2A, TLR2B, TLR4 and TLR5). The level of positive selection was low in endosomal TLRs which bind structurally more conservative oligonucleotide ligands (TLR3, TLR7 and TLR21). Positive selection also appears to act more on three-domain than on single-domain TLRs (except for TLR5 that is under very strong positive selection in birds). We also compared the PSS detected in this study with those previously described on an interspecific level in birds and mammals and with all sites previously identified as functionally relevant in TLRs to show strongest evidence for functional effect of the predicted PSS in TLR1 [TLR1B], TLR2A, TLR4 and TLR5. In agreement with the hypothesis that the variation in the TLR ligands is a driving force for selection in TLRs, non-conservative substitutions with the potential to dramatically change surface physicochemical properties were found mainly in two TLRs (TLR2A and TLR4) with highly variable ligands known in mammals. Altogether, our results indicate strong positive selection driving TLR evolution in birds. To better understand the significance of this adaptive evolution in avian *TLR* genes, further research would benefit from both *in silico* structural modelling allowing closer prediction of the positively selected physicochemical changes and functional testing of the variant effects in model *in vitro* systems.

Materials and Methods

Dataset

To create our dataset, we used sequence data publicly available for up to 63 avian species per gene representing all orders of Neoaves (Supplementary Material 2: Table S23). Most of the *TLR* sequences were extracted from the whole-genome data generated by the Avian Phylogenomics Consortium (http://avian.genomics.cn/en/; Zhang et al. 2014a), genomes included in the B10K Project (Avianbase; http://b10k.genomics.cn/; Eöry et al. 2015). The nucleotide sequences of all avian *TLRs* were obtained by blasting (BLAST v 2.2.25+, NCBI, Zhang et al. 2000; blastn settings: E=0.1, hits with the highest score and lowest E were accepted) the reference *TLR* sequences of chicken and zebra finch (for sequence ID number see Supplementary Material 1: Table S14) against the CDS database of all avian whole-genome-sequences of the species included in the first B10K study (Zhang et al. 2014a). In cases where the blast search in the CDS databases was not successful, we ran blat search against the genomic scaffolds (e.g. the case of *TLR5* pseudogenes; see Supplementary Material 1: Text S3 and Table S15; settings: tile size = 11, step size = 5, allowing one mismatch in tile, the number of repetitions of a tile = 1,000,000). In several avian species, where *TLRs* were previously sequenced, the sequences were found using on-line Web BLAST search (blastn searching cds database with default settings; https://blast.ncbi.nlm.nih.gov/Blast.cgi; accessed in March 2013) and downloaded directly from the GenBank nucleotide database (Benson et al. 2013). The list of NCBI accession numbers of the sequences used is given in Supplementary Material 2: Table S23. Basic description of the *TLR* CDS analysed is provided in Supplementary Material 1: Text S4, Table S16, Table S17 and more detailed in Supplementary Material 2: Table S25.

Multiple sequence alignment

First, all CDSs were translated to extract the protein sequences of all representatives of each TLR family member. Then, the multiple amino acid sequence alignment was done for each TLR separately using the ClustalW alignment tool implemented in Geneious v. 9.0.4 (Biomatters Limited; Kearse et al. 2012), or using MAFFT v. 6.850 (Katoh and Standley 2013) in the case of the duplicated genes from the vertebrate *TLR1* family. For the construction of nucleotide codon alignments corresponding to the protein sequence alignments we used the PAL2NAL webtool v. 14 (http://www.bork.embl.de/pal2nal/; Suyama et al. 2006). All created multiple alignments are shown in Supplementary Material 10.

Gene conversion analysis

The occurrence of gene conversion was statistically tested on nucleotide sequence alignment of all duplicated genes (*TLR1*, *TLR2* and *TLR7*) using GENECONV v. 1.81 (S. A. Sawyer, Washington

University in St. Louis, http://www.math.wustl.edu/~sawyer/geneconv/). Full program setting is provided for all investigated genes in Supplementary Material 3.

Phylogenetic tree analyses

Phylogenetic analysis was done only in the duplicated avian *TLRs* (i.e. in *TLR1*, *TLR2* and *TLR7*), also including other vertebrate taxa, i.e., mammals, reptiles, amphibians and fishes (involved species and their sequences IDs are listed in Supplementary Material 2: Table S24). For the *TLR1* family, the phylogenetic analysis was based on the sequence alignment of non-converted amino acid regions only. Amino acid sequences were used instead of nucleotide sequences to avoid the biasing effect of rapid evolution on the third codon positions on broad evolutionary scales (i.e. higher vertebrate taxa). For the phylogenetic analysis we used two approaches: maximum likelihood calculated in PhyML v. 3.0 software package (Bootstrap: 1000; Tree type: SPR&NNI; Substitution model: LG; Guindon et al. 2010) and Bayesian estimation of phylogeny calculated using MrBayes v. 3.2.1 (number of generations: 1000; burn-in fraction was set to default of 25%; the critical value for topological convergence diagnostic was 0.01; the best suited aa model for TLR1: Fixed(Jones) and for TLR2: Fixed(Wag); Ronquist et al. 2012). Schematic phylogenetic trees for visualisation of *TLR7* duplication (Fig. 2) and *TLR5* pseudogenisation (Fig. 3) were constructed using previously published avian phylogeny (Jarvis et al. 2014). All trees were graphically adjusted in FigTree v1.3.1 (A. Rambaut, University of Edinburgh, UK; http://tree.bio.ed.ac.uk/software/figtree/).

Copy number variation analysis

To verify the increased number of *TLR7* copies in selected passerine species we performed a qPCR copy number variation (CNV) analysis. Tissue samples of four model species (*Ficedula albicollis*, *Pseudopodoces humilis*, *Taeniopygia guttata* and *Zonotrichia albicollis*) used for this analysis were obtained from various genetic banks (for details see Supplementary Material 1: Table S18). DNA was extracted using the DNeasy Blood and Tissue Kit (QIAGEN) and stored at -20 °C. As reference single copy genes, we used *TLR3* and *TLR4*. Primers were designed to amplify a conserved region of a similar length for all studied genes (for details see Supplementary Material 1: Table S19). The specificity of the primers was previously verified by Sanger sequencing (Applied Biosystems® 3130xl Genetic Analyzer) of a broader surrounding region of each gene in all investigated species (for PCR conditions see Supplementary Material 1: Table S20; NCBI accession numbers are listed in Supplementary Material 1: Table S21). Each sample was run in triplicate in LightCycler 480 Instrument II (Roche) using EvaGreen® Dye (Biotum; Mao et al. 2007). The qPCR efficiency was calculated based on a dilution series (5-times dilution) for each gene and sample in LightCycler® 480

software v1.5.1 using both 2nd Derivate function and automatic Fit Point method (the values measured are shown in Supplementary Material 1: Table S4). The *TLR7* copy numbers were then calculated based on a modified version of the formula proposed by Pfaffl (2001; Equation 1, where Eff stands for the PCR efficiency and Cp stands for the crossing point).

$$\mathbf{R} = \mathbf{2} * \frac{\mathbf{Eff}_{\mathrm{TLR7}}{}^{-\mathbf{Cp}_{\mathrm{TLR7}}}}{\mathbf{Eff}_{\mathrm{TLR3}}{}^{-\mathbf{Cp}_{\mathrm{TLR3}}} + \mathbf{Eff}_{\mathrm{TLR4}}{}^{-\mathbf{Cp}_{\mathrm{TLR4}}}} \qquad \text{Equation 1}$$

Positive selection analysis and estimates of conservativeness of amino acid substitutions

For the detection of selective pressures acting on each avian *TLR*, the codon alignment generated by PAL2NAL tool (http://www.bork.embl.de/pal2nal/; Suyama et al. 2006) was used to ensure correct alignment of codons. All regions involving gaps were removed before the analysis and tested separately. The problem of missing sequence data did not impact our estimates since the number of sequences sampled was not too small in any of the TLRs and thus the dN/dS ratios could have been estimated. The position numbering of PSS followed the chicken reference sequence (for NCBI IDs see Supplementary Material 1: Table S14). To test for positive selection acting on individual residues at the interspecific level in avian TLRs we used two methods based on the hierarchical Bayes (Bayes Empirical Bayes, BEB) approach implementing the Markov chain Monte Carlo routine - PAML (Phylogenetic Analysis by Maximum Likelihood; Yang 2007) and FUBAR (A Fast, Unconstrained Bayesian AppRoximation for Inferring Selection; Murrell et al. 2013). Being based on unrelated preconditions, these two tests provide independent estimates of positive selection. In PAML (Version 4.7), the codon-based substitution models (codeml) using comparison of neutral M8a (beta&ω=1) with alternative M8 (beta&ω) model were adopted. The likelihood ratio test (LRT) for comparison of two nested models was calculated using the chi-square approximation: X^2 = 2 x (lnLM8 - lnLM8a), where LM8 and LM8a are the likelihood values. The degrees of freedom (df) were established as the difference in the numbers of parameters in used models (for details see Supplementary Material 1: Table S10). If the LRT is significant (≤0.05), positive selection is considered to be detected. The BEB approach (Yang 2007) was then used to determine site specific posterior probabilities indicating positive selection (≥0.9) at specific codons. The phylogenetic tree needed for PAML analysis was constructed based on the previously published avian phylogeny (Jarvis et al. 2014). FUBAR (Fast Unconstrained Bayesian AppRoximation) analysis was performed at the Datamonkey server (http://www.datamonkey.org/; accessed in July 2014; Pond and Frost 2005) with the significance level of posterior probability established by default to 0.9. The FUBAR algorithm was used because it

is more robust and much faster than other available selection tests, which are based on the random effect likelihood (REL; Murrell et al. 2013) methods. The degree of dissimilarity in biochemical properties of amino acid substitutions was tested using the PRIME tool (PRoperty Informed Model of Evolution; accessed in July 2014) available at the Datamonkey server (Pond and Frost 2005). This tool builds on the same conceptual frameworks as MEME (Murrell et al. 2012), but allows the non-synonymous substitution rate β to depend not only on the site in question, but also on what type of residues are being exchanged. Both predefined sets of five amino-acid composite properties were used for PRIME analysis: i) Polarity index, Secondary structure factor, Volume, Refractivity/Heat Capacity and Charge/Iso-electric point (Atchley et al. 2005) and ii) Chemical Composition, Polarity, Volume, Iso-electric point and Hydropathy (Conant et al. 2007) on the significant level of posterior probabilities ≥0.9. Amino acid physicochemical properties (chemistry, charge and hydrophobicity) at all PSS were graphically visualised using a web-based application Weblogo v. 3.5 (http://weblogo.threeplusone.com/create.cgi; Crooks et al. 2004).

We compared the PSS identified in this study with the results of other studies that focused on avian and mammalian TLR evolution identifying positive selection at the interspecific level (Nakajima et al. 2008; Vinkler et al. 2009; Wlasiuk et al. 2009; Wlasiuk and Nachman 2010; Alcaide and Edwards 2011; Areal et al. 2011; Huang et al. 2011; Shen et al. 2012; Fornuskova et al. 2013; Grueber et al. 2014; Vinkler et al. 2014; Wang et al. 2016a) and studies that described the functionally relevant residues for TLR1 (Jin et al. 2007; Omueti et al. 2007), TLR2 (Underhill et al. 1999; Lorenz et al. 2000; Xu et al. 2000; Kang and Chae 2001; Tao et al. 2002; Gautam et al. 2006; Kang et al. 2009), TLR3 (Sarkar et al. 2003; de Bouteiller et al. 2005; Choe et al. 2005; Bell et al. 2006; Sun et al. 2006; Ranjith-Kumar et al. 2007; Liu et al. 2008; Pirher et al. 2008; Luo et al. 2012; Mineev et al. 2014), TLR4 (Poltorak et al. 1998; Ronni et al. 2003; Nishitani et al. 2006; Kim et al. 2007; Walsh et al. 2008; Park et al. 2009; Resman et al. 2009; Meng et al. 2010; Ohto et al. 2012a; Ohto et al. 2012b; Garate and Oostenbrink 2013; Paramo et al. 2013; Scior et al. 2013; Wang et al. 2016c), TLR5 (Jacchieri et al. 2003; Andersen-Nissen et al. 2007; Keestra et al. 2008; Yoon et al. 2012; Ivicak-Kocjan et al. 2013; Song et al. 2017), TLR7 (Wei et al. 2009; Yu et al. 2013; Tseng et al. 2014; Gentile et al. 2015; Gupta et al. 2016; Zhang et al. 2016), TLR10 (Hasan et al. 2005; Nyman et al. 2008; Guan et al. 2010; Jang and Park 2014), TLR15 (Wang et al. 2016a) and TLR21 (Keestra et al. 2010).

Protein structure modelling

To predict 3D structures of all avian TLRs, the I-TASSER v. 5.0 server (https://zhanglab.ccmb.med.umich.edu/I-TASSER/; Roy et al. 2010) was used. Since all TLRs are transmembrane proteins, the ECD and ICD (and in the case of TLR3 also TM region) were modelled

separately, always based on the chicken reference sequence (for NCBI IDs see the Supplementary Material 1: Table S14). The domains were identified by SMART v. 7.0 web tool (http://smart.embl-heidelberg.de/; Letunic and Bork 2017), the amino acid ranges of ECD and ICD for each TLR are provided in Supplementary Material 1: Table S22. The I-TASSER model with the highest C value reflecting the confidence score for estimating the quality of predicted models was always downloaded and used for further analysis. The graphical visualisation of important residues was then done using the PyMOL Molecular Graphics System (Version 1.7.6, Schrödinger, LLC).

Assessing function of positively selected sites

The list of the previously reported functionally important positions as well as PSS detected in other interspecific studies for all TLRs were obtained by a detailed review of the published literature (for the complete list of references see Supplementary Material 6: Table S27). The distance of any PSS detected in our study from these previously described functionally important residues was measured on the 3D structural models of TLRs (obtained in previous step) in the PyMOL Molecular Graphics System (Version 1.7.6, Schrödinger, LLC) using python command iterate and plugin distancetoatom, where PSS lying in distance closer to 5 Å were considered as closely connected to the functionally important residues, i.e. having potential influence on the receptor function.

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Authors' contributions

The authors' contribution to this paper was as follows: HV (70%) – study design, performed all given analyses, prepared all output files, wrote the first draft of the manuscript; MWGD (5%) – involvement in BLAST of genomic databases and PAML analysis; DWB (10%) – supervision of MWGD and study design and MV (15%) – study design, revised the manuscript. All authors contributed by their comments to the manuscript preparation, read and approved the final manuscript.

Tables

Table 1: The number of positively selected sites in avian TLRs.

	Species[a]	aa length[b]	PSS[c]	PSS/TLR[d] (%)
TLR10 [TLR1A]	45	794	**31**	3.9
TLR1 [TLR1B]	44	638	**37**	5.8
TLR2A	40	793	**43**	5.4
TLR2B	42	781	**35**	4.5
TLR3	51	895	**19**	2.1
TLR4	54	843	**38**	4.5
TLR5	46	861	**45**	5.2
TLR7	51	1041	**31**	3.0
TLR15	53	868	**24**	2.8
TLR21	14	907	**3**	0.3

a - number of species (one sequence per species)

b - the protein sequence length in reference chicken TLRs (NCBI accession numbers are listed in Supplementary Material 1: Table S14)

c - number of positively selected sites detected in investigated species per each gene

d - the percentage of PSS per whole receptor amino acid sequence

Figures

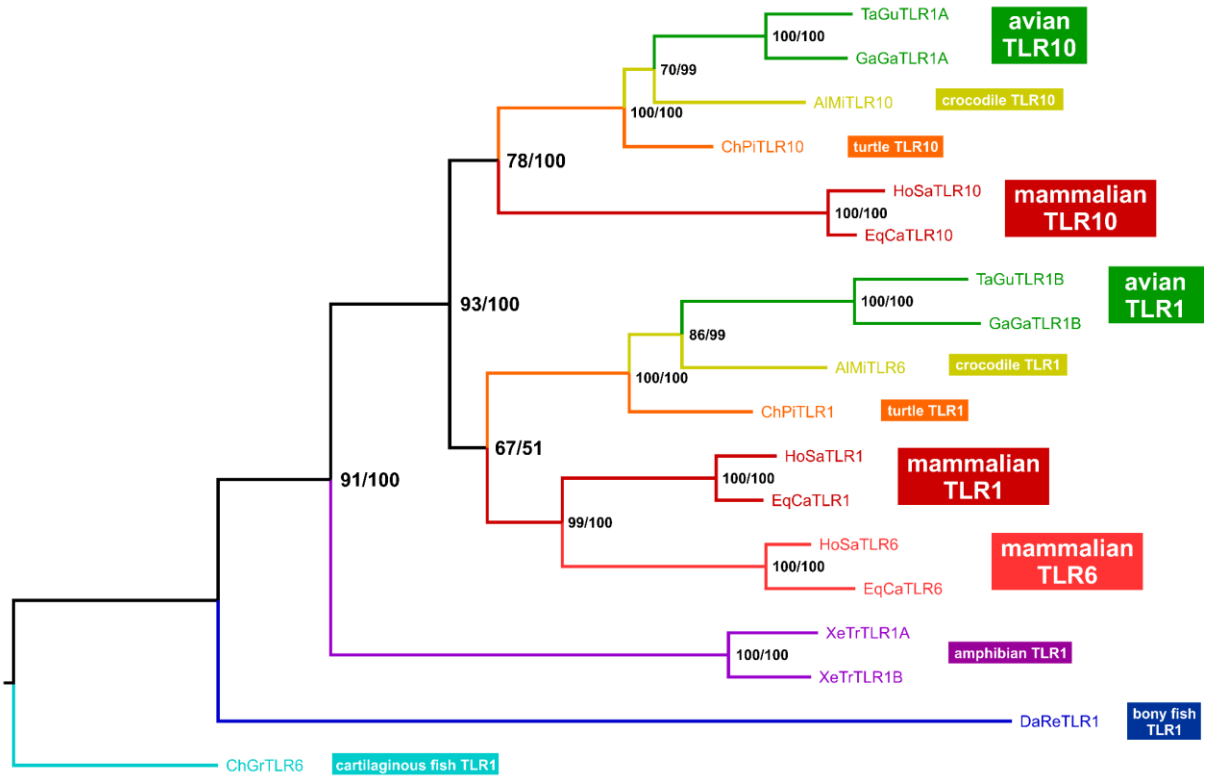

Fig. 1: Phylogenetic tree based on non-converted regions of *TLR1* subfamily members. The bootstrap values of maximum likelihood analysis obtained using PhyML and the posterior probability of Bayesian analysis obtained using MrBayes (in percentage per each node) are provided. Birds are represented by zebra finch (TaGu, *Taeniopygia guttata*) and chicken (GaGa, *Gallus gallus*), crocodiles by alligator (AlMi, *Alligator mississippiensis*), turtles by painted turtle (ChPi, *Chrysemys picta*), mammals by human (HoSa, *Homo sapiens*) and horse (EqCa, *Equus caballus*), amphibians by clawed frog (XeTr, *Xenopus tropicalis*), bony fish by zebrafish (DaRe, *Danio rerio*) and cartilaginous fish by shark (ChGr, *Chiloscyllium griseum*). The analysis was performed using a single amino acid sequence per TLR and species. Based on the results we suggest renaming TLR1A to TLR10 and TLR1B to TLR1 in birds.

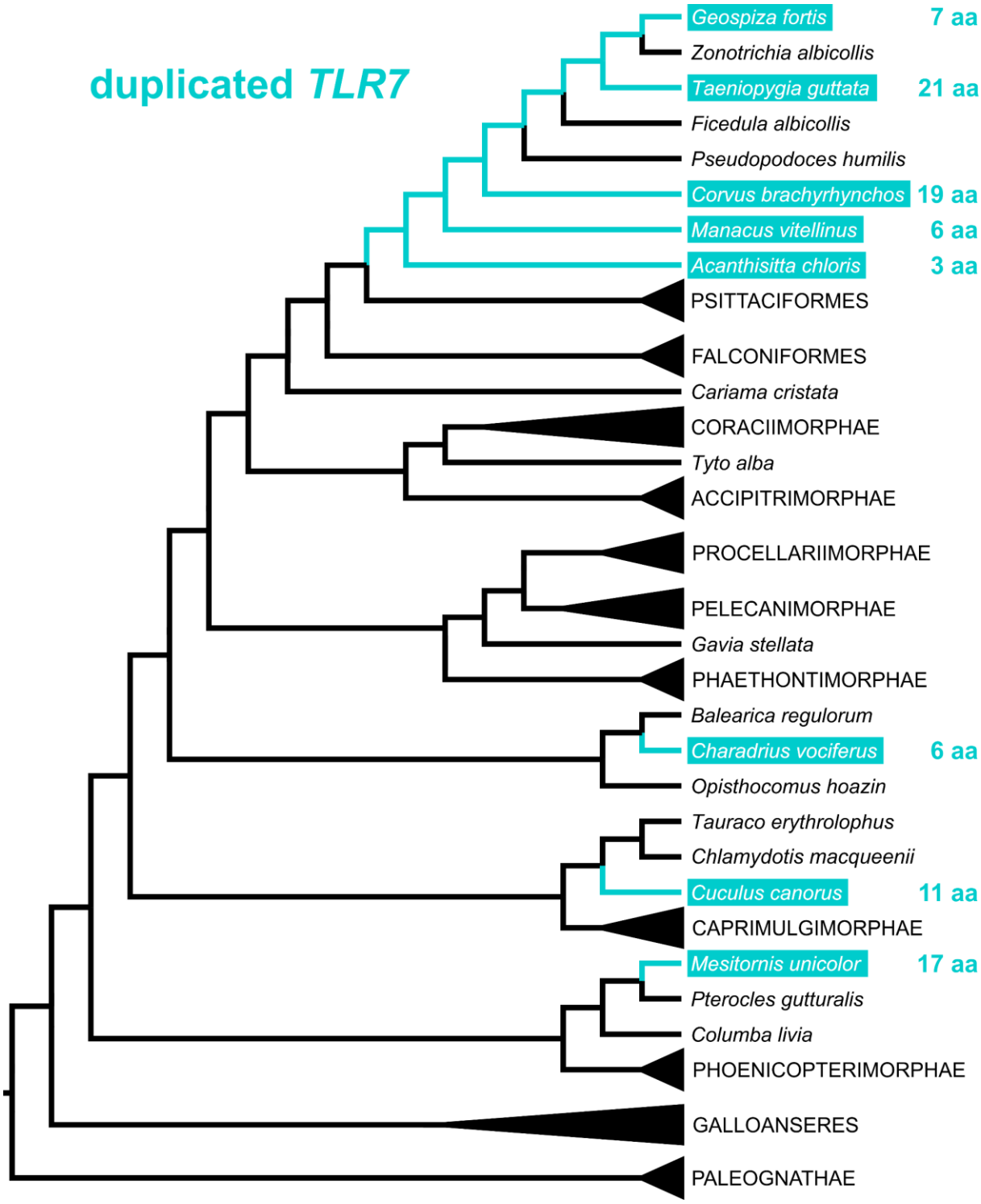

Fig. 2: Avian *TLR7* duplication. In the schematic avian phylogenetic tree the species with duplicated *TLR7* are highlighted in blue rectangles. The numbers of amino acid substitutions distinguishing the two copies of the duplicated *TLR7* are shown behind the species name. The analysis was performed using a single sequence per gene and species.

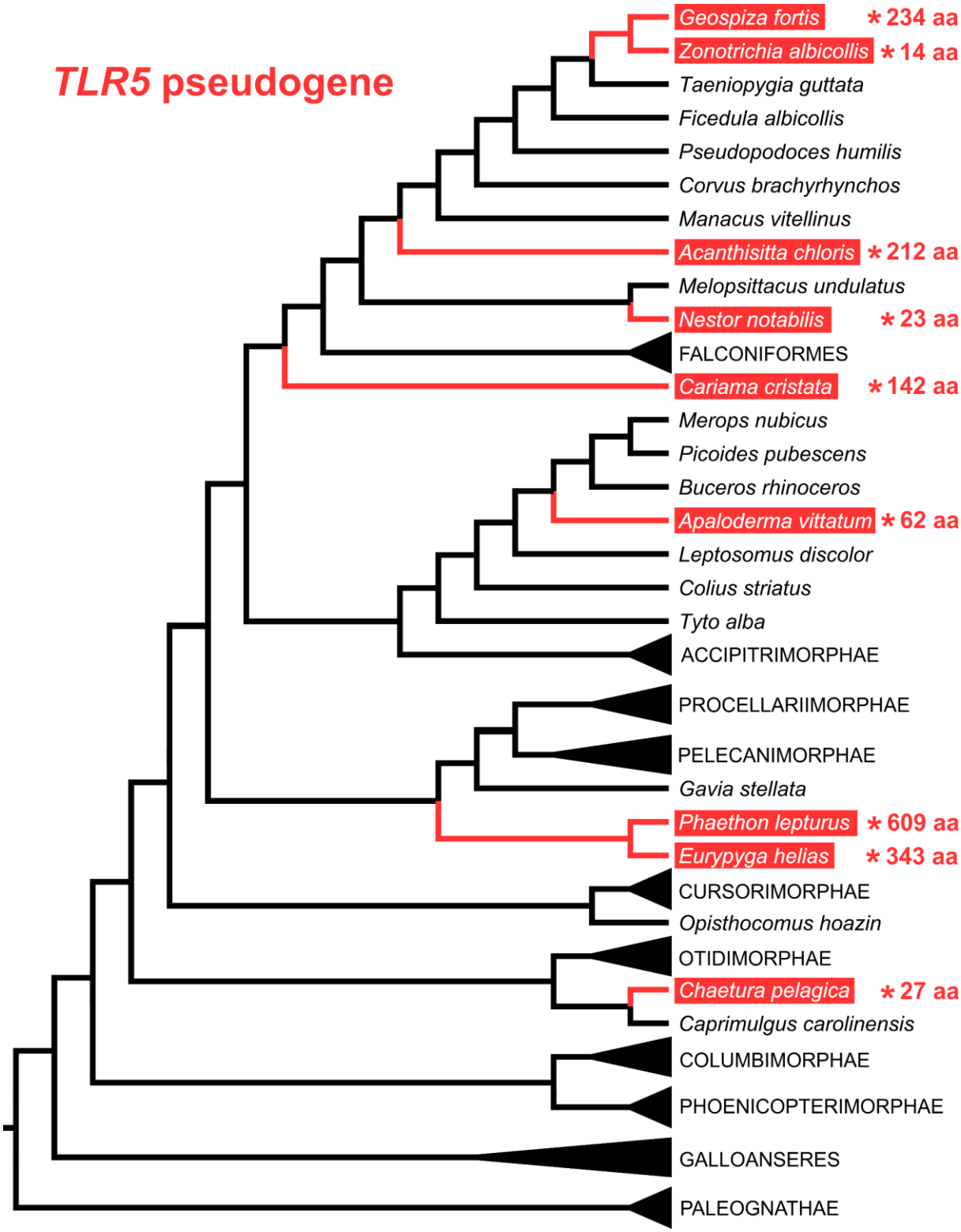

Fig. 3: *TLR5* pseudogenisation in birds. Species possessing only *TLR5* pseudogene are highlighted in red rectangles within the schematic representation of avian phylogenetic tree. The position of the first stop codon is indicated by the number provided behind the species name (position numbering according to the chicken reference). The analysis was performed using a single sequence per gene and species.

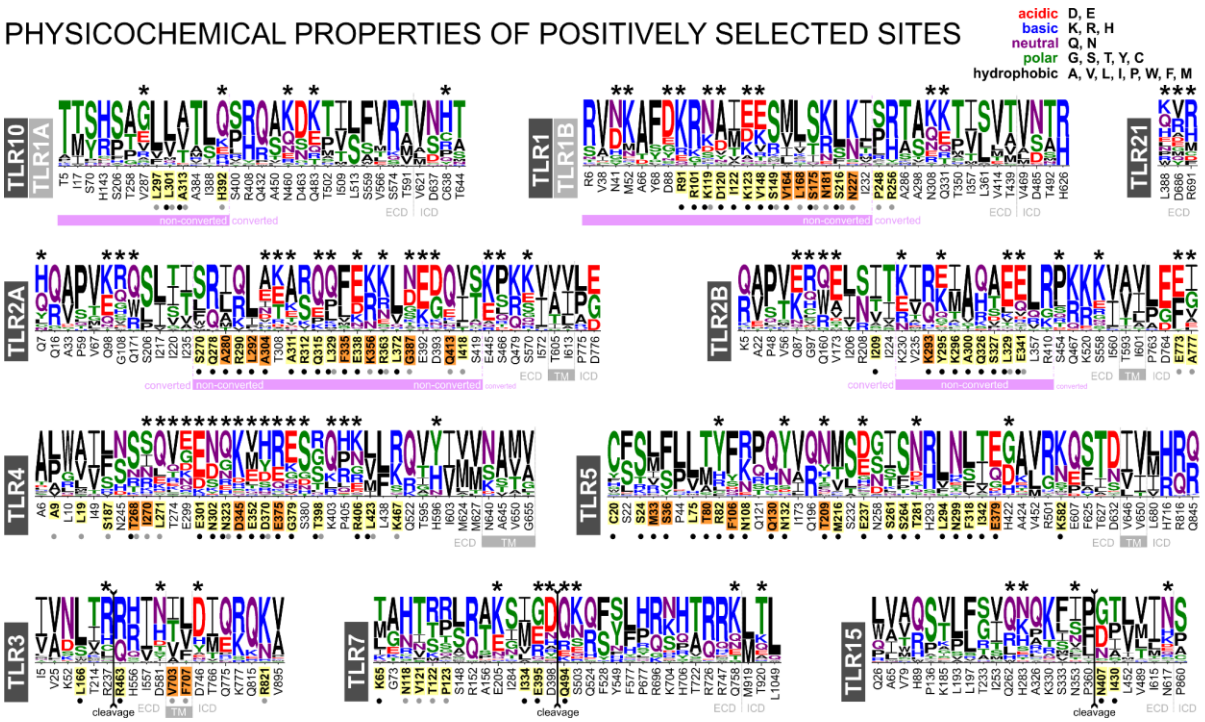

Fig. 4: Physicochemical properties of the positively selected sites (PSS). All PSS are shown in all avian TLRs - amino acid substitutions are coloured according to their physicochemical properties: acidic in red, basic in blue, neutral in purple, polar in green and hydrophobic in black. The size of an letter corresponds to the procentual proportion of that particular amino acid within the sequence alignment. The numbering is adopted from reference chicken TLRs (for NCBI IDs see Supplementary Material 1: Table S14). PSS which correspond to functionaly important residues (black dot - ligand binding; grey dot – dimerization) are highlighted in bold and orange (identical site) or yellow (topological proximity closer than 5 Å from a functionaly important residue). Ectodomain (ECD), intracellular domain (ICD) and transmembrane (TM) region are visualised; non-converted region in TLR1/2 is highlighted in pink; cleavage site in TLR3, TLR7 and TLR15 is indicated by a black line tipped with arrows (Supplementary Material 1: Table S11 and Text S1). Non-conservative PSS are marked by stars (Supplementary Material 1: Table S12).

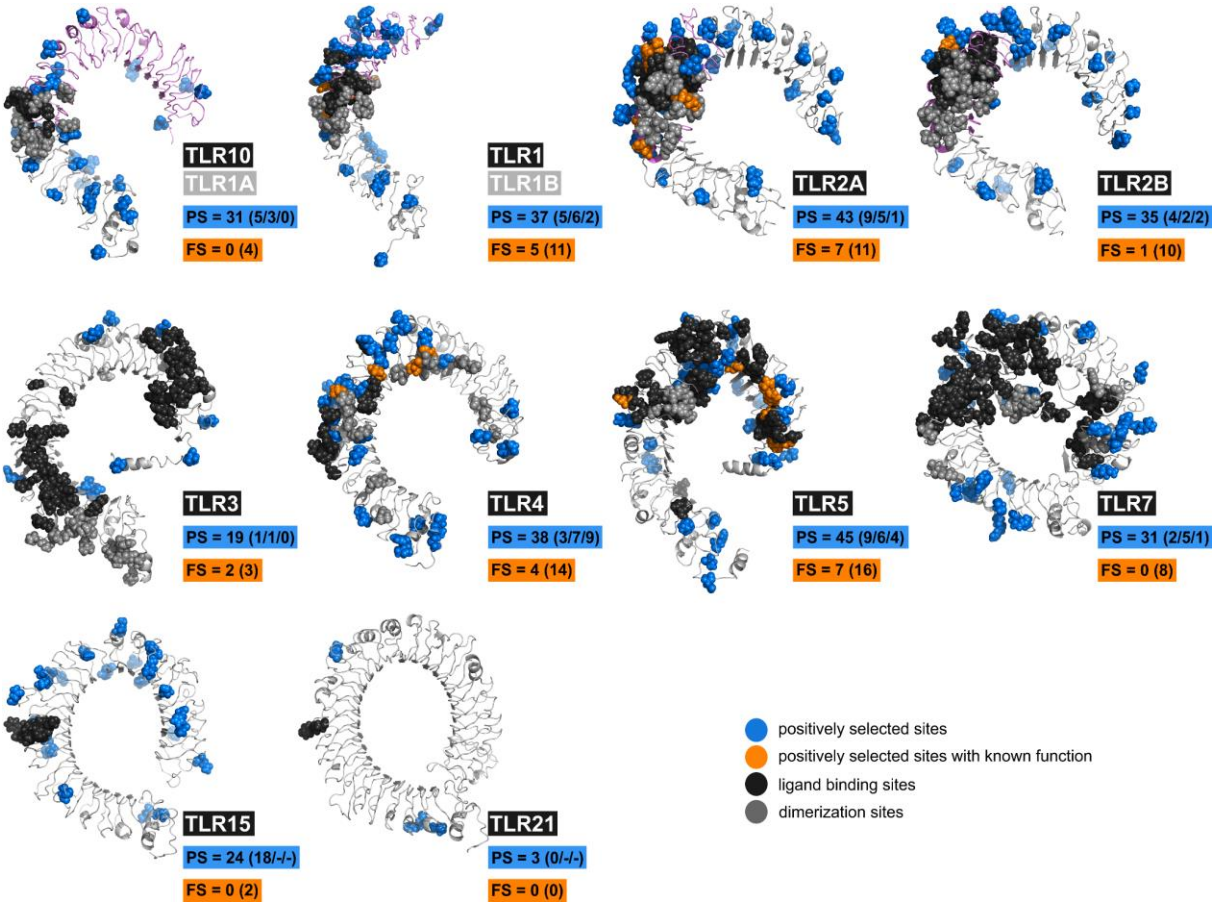

Fig. 5: Positively selected sites and functionaly important sites visualised on 3D extracellular domain structures of avian TLRs. PSS detected in this study are shown in blue. By orange coloration are highlighted the PSS identified at sites with previously described function. Other previously reported functionaly important residues are highlighted in black (ligand binding residues) or in gray (dimerization residues). The total numbers of PSS for each TLR are shown in blue rectangles, where in parentheses are numbers of PSS detected also in other avian/mammalian/both studies (for references see Supplementary Material 6: Table S27). The numbers of PSS with previously described function are provided in orange rectangles, where the number of PSS in topological proximity <5 Å is shown in parentheses. For more detailed information (including ICD and TM) see Supplementary Material 9.

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